

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,662
Source: IFWP
Date Processed by STIC: 5/30/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/579,662

CRF Edit Date: 5/30/06
Edited by: ME

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

J
___ Other: corrected <141> line



IFWP

RAW SEQUENCE LISTING

DATE: 05/30/2006

PATENT APPLICATION: US/10/579,662

TIME: 16:07:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\05302006\J579662.raw

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3 <110> APPLICANT: ELENA FEINSTEIN et al.
5 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF KIDNEY FIBROSIS AND OTHER
FIBROTIC
6      DISEASE
8 <130> FILE REFERENCE: 71541-A-PCT-US; 133/PCT1-US1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,662
C--> 11 <141> CURRENT FILING DATE: 2006-05-17
13 <150> PRIOR APPLICATION NUMBER: 60/520,935
14 <151> PRIOR FILING DATE: 2003-11-17
16 <150> PRIOR APPLICATION NUMBER: PCT/IL 2004/001049
17 <151> PRIOR FILING DATE: 2004-11-16
19 <160> NUMBER OF SEQ ID NOS: 8
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3225
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(3225)
33 <400> SEQUENCE: 1
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38 att gct gct gac atg agt aat atc ata gaa aat ctg gac acg cgg gaa      96
39 Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg Glu
40          20          25          30
42 ctc cac ttt gag gga gag gag gta gac tac gac gtg tct ccc agc gat      144
43 Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp
44          35          40          45
46 ccc aag ata caa gaa gtg tat atc cct ttc tct gct att tat aac act      192
47 Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr
48          50          55          60
50 caa gga ttt aag gag cct aat ata cag acg tat ctc tcc ggc tgt cca      240
51 Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro
52 65          70          75          80
54 ata aaa gca caa gtt ctg gaa gtg gaa cgc ttc aca tct aca aca agg      288
55 Ile Lys Ala Gln Val Leu Glu Val Glu Arg Phe Thr Ser Thr Thr Arg
56          85          90          95
58 gta cca agt att aat ctt tac act att gaa tta aca cat ggg gaa ttt      336
59 Val Pro Ser Ile Asn Leu Tyr Thr Ile Glu Leu Thr His Gly Glu Phe
60          100          105          110
62 aaa tgg caa gtt aag agg aaa ttc aag cat ttt caa gaa ttt cac aga      384
63 Lys Trp Gln Val Lys Arg Lys Phe Lys His Phe Gln Glu Phe His Arg

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Input Set : A:\PTO.AMC.txt

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67 Glu Leu Leu Lys Tyr Lys Ala Phe Ile Arg Ile Pro Ile Pro Thr Arg				
68 130	135	140		
70 aga cac acg ttt agg agg caa aac gtc aga gag gag cct cga gag atg				480
71 Arg His Thr Phe Arg Arg Gln Asn Val Arg Glu Glu Pro Arg Glu Met				
72 145	150	155	160	
74 ccc agt ttg ccc cgt tca tct gaa aac atg ata aga gaa gaa caa ttc				528
75 Pro Ser Leu Pro Arg Ser Ser Glu Asn Met Ile Arg Glu Glu Gln Phe				
76 165	170	175		
78 ctt ggt aga aga aaa caa ctg gaa gat tac ttg aca aag ata cta aaa				576
79 Leu Gly Arg Arg Lys Gln Leu Glu Asp Tyr Leu Thr Lys Ile Leu Lys				
80 180	185	190		
82 atg ccc atg tat aga aac tat cat gcc aca aca gag ttt ctt gat ata				624
83 Met Pro Met Tyr Arg Asn Tyr His Ala Thr Thr Glu Phe Leu Asp Ile				
84 195	200	205		
86 agc cag ctg tct ttc atc cat gat ttg gga cca aag ggc ata gaa ggt				672
87 Ser Gln Leu Ser Phe Ile His Asp Leu Gly Pro Lys Gly Ile Glu Gly				
88 210	215	220		
90 atg ata atg aaa aga tct gga gga cac aga ata cca ggc ttg aat tgc				720
91 Met Ile Met Lys Arg Ser Gly Gly His Arg Ile Pro Gly Leu Asn Cys				
92 225	230	235	240	
94 tgt ggt cag gga aga gcc tgc tac aga tgg tca aaa aga tgg tta ata				768
95 Cys Gly Gln Gly Arg Ala Cys Tyr Arg Trp Ser Lys Arg Trp Leu Ile				
96 245	250	255		
98 gtg aaa gat tcc ttt tta ttg tat atg aaa cca gac agc ggt gcc att				816
99 Val Lys Asp Ser Phe Leu Leu Tyr Met Lys Pro Asp Ser Gly Ala Ile				
100 260	265	270		
102 gcc ttc gtc ctg ctg gta gac aaa gaa ttc aaa att aag gtg ggg aag				864
103 Ala Phe Val Leu Leu Val Asp Lys Glu Phe Lys Ile Lys Val Gly Lys				
104 275	280	285		
106 aag gag aca gaa acg aaa tat gga atc cga att gat aat ctt tca agg				912
107 Lys Glu Thr Glu Thr Lys Tyr Gly Ile Arg Ile Asp Asn Leu Ser Arg				
108 290	295	300		
110 aca ctt att tta aaa tgc aac agc tat aga cat gct cgg tgg tgg gga				960
111 Thr Leu Ile Leu Lys Cys Asn Ser Tyr Arg His Ala Arg Trp Trp Gly				
112 305	310	315	320	
114 ggg gct ata gaa gaa ttc atc cag aaa cat ggc acc aac ttt ctc aaa				1008
115 Gly Ala Ile Glu Glu Phe Ile Gln Lys His Gly Thr Asn Phe Leu Lys				
116 325	330	335		
118 gat cat cga ttt ggg tca tat gct gct atc caa gag aat gct tta gct				1056
119 Asp His Arg Phe Gly Ser Tyr Ala Ala Ile Gln Glu Asn Ala Leu Ala				
120 340	345	350		
122 aaa tgg tat gtt aat gcc aaa gga tat ttt gaa gat gtg gca aat gca				1104
123 Lys Trp Tyr Val Asn Ala Lys Gly Tyr Phe Glu Asp Val Ala Asn Ala				
124 355	360	365		
126 atg gaa gag gca aat gaa gag att ttt atc aca gac tgg tgg ctg agt				1152
127 Met Glu Glu Ala Asn Glu Glu Ile Phe Ile Thr Asp Trp Trp Leu Ser				
128 370	375	380		

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DATE: 05/30/2006

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TIME: 16:07:42

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131	Pro	Glu	Ile	Phe	Leu	Lys	Arg	Pro	Val	Val	Glu	Gly	Asn	Arg	Trp	Arg	
132	385					390						395				400	
134	ttg	gac	tgc	att	ctt	aaa	cga	aaa	gca	caa	caa	gga	gtg	agg	atc	ttc	1248
135	Leu	Asp	Cys	Ile	Leu	Lys	Arg	Lys	Ala	Gln	Gln	Gly	Val	Arg	Ile	Phe	
136					405					410					415		
138	ata	atg	ctc	tac	aaa	gag	gtg	gaa	ctc	gct	ctt	ggc	atc	aat	agt	gaa	1296
139	Ile	Met	Leu	Tyr	Lys	Glu	Val	Glu	Leu	Ala	Leu	Gly	Ile	Asn	Ser	Glu	
140				420					425					430			
142	tac	acc	aag	agg	act	ttg	atg	cgt	cta	cat	ccc	aac	ata	aag	gtg	atg	1344
143	Tyr	Thr	Lys	Arg	Thr	Leu	Met	Arg	Leu	His	Pro	Asn	Ile	Lys	Val	Met	
144			435					440						445			
146	aga	cac	ccg	gat	cat	gtg	tca	tcc	acc	gtc	tat	ttg	tgg	gct	cac	cat	1392
147	Arg	His	Pro	Asp	His	Val	Ser	Ser	Thr	Val	Tyr	Leu	Trp	Ala	His	His	
148		450					455						460				
150	gag	aag	ctt	gtc	atc	att	gac	caa	tgc	gtg	gcc	ttt	gtg	gga	ggg	att	1440
151	Glu	Lys	Leu	Val	Ile	Ile	Asp	Gln	Ser	Val	Ala	Phe	Val	Gly	Gly	Ile	
152	465				470					475						480	
154	gac	ctg	gcc	tat	gga	agg	tgg	gac	gac	aat	gag	cac	aga	ctc	aca	gac	1488
155	Asp	Leu	Ala	Tyr	Gly	Arg	Trp	Asp	Asp	Asn	Glu	His	Arg	Leu	Thr	Asp	
156				485						490					495		
158	gtg	ggc	agt	gtg	aag	cgg	gtc	act	tca	gga	ccg	tct	ctg	ggg	tcc	ctc	1536
159	Val	Gly	Ser	Val	Lys	Arg	Val	Thr	Ser	Gly	Pro	Ser	Leu	Gly	Ser	Leu	
160			500						505					510			
162	cca	cct	gcc	gca	atg	gag	tct	atg	gaa	tcc	tta	aga	ctc	aaa	gat	aaa	1584
163	Pro	Pro	Ala	Ala	Met	Glu	Ser	Met	Glu	Ser	Leu	Arg	Leu	Lys	Asp	Lys	
164			515					520						525			
166	aat	gag	cct	gtt	caa	aac	cta	ccc	atc	cag	aag	agt	att	gat	gat	gtg	1632
167	Asn	Glu	Pro	Val	Gln	Asn	Leu	Pro	Ile	Gln	Lys	Ser	Ile	Asp	Asp	Val	
168		530					535							540			
170	gat	tca	aaa	ctg	aaa	gga	ata	gga	aag	cca	aga	aag	ttc	tcc	aaa	ttt	1680
171	Asp	Ser	Lys	Leu	Lys	Gly	Ile	Gly	Lys	Pro	Arg	Lys	Phe	Ser	Lys	Phe	
172	545				550					555						560	
174	agt	ctc	tac	aag	cag	ctc	cac	agg	cac	cac	ctg	cac	gac	gca	gat	agc	1728
175	Ser	Leu	Tyr	Lys	Gln	Leu	His	Arg	His	His	Leu	His	Asp	Ala	Asp	Ser	
176				565						570					575		
178	atc	agc	agc	att	gac	agc	acc	tcc	agt	tat	ttt	aat	cac	tat	aga	agt	1776
179	Ile	Ser	Ser	Ile	Asp	Ser	Thr	Ser	Ser	Tyr	Phe	Asn	His	Tyr	Arg	Ser	
180			580						585					590			
182	cat	cac	aat	tta	atc	cat	ggg	tta	aaa	ccc	cac	ttc	aaa	ctc	ttt	cac	1824
183	His	His	Asn	Leu	Ile	His	Gly	Leu	Lys	Pro	His	Phe	Lys	Leu	Phe	His	
184			595				600							605			
186	ccg	tcc	agt	gag	tct	gag	caa	gga	ctc	act	aga	cct	cat	gct	gat	acc	1872
187	Pro	Ser	Ser	Glu	Ser	Glu	Gln	Gly	Leu	Thr	Arg	Pro	His	Ala	Asp	Thr	
188		610					615							620			
190	ggg	tcc	atc	cgt	agt	tta	cag	aca	ggg	gtg	gga	gag	ctg	cat	ggg	gaa	1920
191	Gly	Ser	Ile	Arg	Ser	Leu	Gln	Thr	Gly	Val	Gly	Glu	Leu	His	Gly	Glu	
192	625					630					635					640	
194	acc	aga	ttc	tgg	cat	gga	aag	gac	tac	tgc	aat	ttc	gtc	ttc	aaa	gac	1968

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TIME: 16:07:42

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Output Set: N:\CRF4\05302006\J579662.raw

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196					645					650					655		
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199	Trp	Val	Gln	Leu	Asp	Lys	Pro	Phe	Ala	Asp	Phe	Ile	Asp	Arg	Tyr	Ser	
200				660					665					670			
202	acg	ccc	cgg	atg	ccc	tgg	cat	gac	att	gcc	tct	gca	gtc	cac	ggg	aag	2064
203	Thr	Pro	Arg	Met	Pro	Trp	His	Asp	Ile	Ala	Ser	Ala	Val	His	Gly	Lys	
204			675					680					685				
206	gcg	gct	cgt	gat	gtg	gca	cgt	cac	ttc	atc	cag	cgc	tgg	aac	ttc	aca	2112
207	Ala	Ala	Arg	Asp	Val	Ala	Arg	His	Phe	Ile	Gln	Arg	Trp	Asn	Phe	Thr	
208		690					695				700						
210	aaa	att	atg	aaa	tca	aaa	tat	cgg	tcc	ctt	tct	tat	cct	ttt	ctg	ctt	2160
211	Lys	Ile	Met	Lys	Ser	Lys	Tyr	Arg	Ser	Leu	Ser	Tyr	Pro	Phe	Leu	Leu	
212	705					710				715					720		
214	cca	aag	tct	caa	aca	aca	gcc	cat	gag	ttg	aga	tat	caa	gtg	cct	ggg	2208
215	Pro	Lys	Ser	Gln	Thr	Thr	Ala	His	Glu	Leu	Arg	Tyr	Gln	Val	Pro	Gly	
216				725					730				735				
218	tct	gtc	cat	gct	aac	gta	cag	ttg	ctc	cgc	tct	gct	gct	gat	tgg	tct	2256
219	Ser	Val	His	Ala	Asn	Val	Gln	Leu	Leu	Arg	Ser	Ala	Ala	Asp	Trp	Ser	
220			740					745				750					
222	gct	ggt	ata	aag	tac	cat	gaa	gag	tcc	atc	cac	gcc	gct	tac	gtc	cat	2304
223	Ala	Gly	Ile	Lys	Tyr	His	Glu	Glu	Ser	Ile	His	Ala	Ala	Tyr	Val	His	
224		755					760				765						
226	gtg	ata	gag	aac	agc	agg	cac	tat	atc	tat	atc	gaa	aac	cag	ttt	ttc	2352
227	Val	Ile	Glu	Asn	Ser	Arg	His	Tyr	Ile	Tyr	Ile	Glu	Asn	Gln	Phe	Phe	
228		770				775				780							
230	ata	agc	tgt	gct	gat	gac	aaa	ggt	gtg	ttc	aac	aag	ata	ggc	gat	gcc	2400
231	Ile	Ser	Cys	Ala	Asp	Asp	Lys	Val	Val	Phe	Asn	Lys	Ile	Gly	Asp	Ala	
232	785				790				795				800				
234	att	gcc	cag	agg	atc	ctg	aaa	gct	cac	agg	gaa	aac	cag	aaa	tac	cgg	2448
235	Ile	Ala	Gln	Arg	Ile	Leu	Lys	Ala	His	Arg	Glu	Asn	Gln	Lys	Tyr	Arg	
236				805				810					815				
238	gta	tat	gtc	gtg	ata	cca	ctt	ctg	cca	ggg	ttc	gaa	gga	gac	att	tca	2496
239	Val	Tyr	Val	Val	Ile	Pro	Leu	Leu	Pro	Gly	Phe	Glu	Gly	Asp	Ile	Ser	
240			820					825				830					
242	acc	ggc	gga	gga	aat	gct	cta	cag	gca	atc	atg	cac	ttc	aac	tac	aga	2544
243	Thr	Gly	Gly	Gly	Asn	Ala	Leu	Gln	Ala	Ile	Met	His	Phe	Asn	Tyr	Arg	
244			835				840					845					
246	acc	atg	tgc	aga	gga	gaa	aat	tcc	atc	ctt	gga	cag	tta	aaa	gca	gag	2592
247	Thr	Met	Cys	Arg	Gly	Glu	Asn	Ser	Ile	Leu	Gly	Gln	Leu	Lys	Ala	Glu	
248		850				855				860							
250	ctt	ggt	aat	cag	tgg	ata	aat	tac	ata	tca	ttc	tgt	ggt	ctt	aga	aca	2640
251	Leu	Gly	Asn	Gln	Trp	Ile	Asn	Tyr	Ile	Ser	Phe	Cys	Gly	Leu	Arg	Thr	
252	865				870				875				880				
254	cat	gca	gag	ctc	gaa	gga	aac	cta	gta	act	gag	ctt	atc	tat	gtc	cac	2688
255	His	Ala	Glu	Leu	Glu	Gly	Asn	Leu	Val	Thr	Glu	Leu	Ile	Tyr	Val	His	
256				885				890				895					
258	agc	aag	ttg	tta	att	gct	gat	gat	aac	act	ggt	att	att	ggc	tct	gcc	2736
259	Ser	Lys	Leu	Leu	Ile	Ala	Asp	Asp	Asn	Thr	Val	Ile	Ile	Gly	Ser	Ala	

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260          900          905          910
262 aac ata aat gac cgc agc atg ctg gga aag cgt gac agt gaa atg gct      2784
263 Asn Ile Asn Asp Arg Ser Met Leu Gly Lys Arg Asp Ser Glu Met Ala
264          915          920          925
266 gtc att gtg caa gat aca gag act gtt cct tca gta atg gat gga aaa      2832
267 Val Ile Val Gln Asp Thr Glu Thr Val Pro Ser Val Met Asp Gly Lys
268          930          935          940
270 gag tac caa gct ggc cgg ttt gcc cga gga ctt cgg cta cag tgc ttt      2880
271 Glu Tyr Gln Ala Gly Arg Phe Ala Arg Gly Leu Arg Leu Gln Cys Phe
272 945          950          955          960
274 agg gtt gtc ctt ggc tat ctt gat gac cca agt gag gac att cag gat      2928
275 Arg Val Val Leu Gly Tyr Leu Asp Asp Pro Ser Glu Asp Ile Gln Asp
276          965          970          975
278 cca gtg agt gac aaa ttc ttc aag gag gtg tgg gtt tca aca gca gct      2976
279 Pro Val Ser Asp Lys Phe Phe Lys Glu Val Trp Val Ser Thr Ala Ala
280          980          985          990
282 cga aat gct aca att tat gac aag gtt ttc cgg tgc ctt ccc aat gat      3024
283 Arg Asn Ala Thr Ile Tyr Asp Lys Val Phe Arg Cys Leu Pro Asn Asp
284          995          1000          1005
286 gaa gta cac aat tta att cag ctg aga gac ttt ata aac aag ccc      3069
287 Glu Val His Asn Leu Ile Gln Leu Arg Asp Phe Ile Asn Lys Pro
288          1010          1015          1020
290 gta tta gct aag gaa gat ccc att cga gct gag gag gaa ctg aag      3114
291 Val Leu Ala Lys Glu Asp Pro Ile Arg Ala Glu Glu Glu Leu Lys
292          1025          1030          1035
294 aag atc cgt gga ttt ttg gtg caa ttc ccc ttt tat ttc ttg tct      3159
295 Lys Ile Arg Gly Phe Leu Val Gln Phe Pro Phe Tyr Phe Leu Ser
296          1040          1045          1050
298 gaa gaa agc cta ctg cct tct gtt ggg acc aaa gag gcc ata gtg      3204
299 Glu Glu Ser Leu Leu Pro Ser Val Gly Thr Lys Glu Ala Ile Val
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304          1070
307 <210> SEQ ID NO: 2
308 <211> LENGTH: 1074
309 <212> TYPE: PRT
310 <213> ORGANISM: Homo sapiens
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319          20          25          30
322 Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp
323          35          40          45
326 Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr
327          50          55          60
330 Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro
331 65          70          75          80

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,662

DATE: 05/30/2006

TIME: 16:07:43

Input Set : A:\PTO.AMC.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 05/26/2006

PATENT APPLICATION: US/10/579,662

TIME: 08:27:02

Input Set : A:\133-PCT1-US1.ST25.txt

Output Set: N:\CRF4\05262006\J579662.raw

3 <110> APPLICANT: ELENA FEINSTEIN et al.

5 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF KIDNEY FIBROSIS AND OTHER

FIBROTIC

6 DISEASE

8 <130> FILE REFERENCE: 71541-A-PCT-US; 133/PCT1-US1

10 <140> CURRENT APPLICATION NUMBER: US/10/579,662

11 <140> CURRENT APPLICATION NUMBER: Herewith

13

13 <150> PRIOR APPLICATION NUMBER: 60/520,935

14 <151> PRIOR FILING DATE: 2003-11-17

16 <150> PRIOR APPLICATION NUMBER: PCT/IL 2004/001049

17 <151> PRIOR FILING DATE: 2004-11-16

19 <160> NUMBER OF SEQ ID NOS: 8

21 <170> SOFTWARE: PatentIn version 3.2

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 3225

25 <212> TYPE: DNA

26 <213> ORGANISM: Homo sapiens

29 <220> FEATURE:

30 <221> NAME/KEY: CDS

31 <222> LOCATION: (1)..(3225)

33 <400> SEQUENCE: 1

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36 1 5 10 15

38 att gct gct gac atg agt aat atc ata gaa aat ctg gac acg cgg gaa 96

39 Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg Glu

40 20 25 30

42 ctc cac ttt gag gga gag gag gta gac tac gac gtg tct ccc agc gat 144

43 Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp

44 35 40 45

46 ccc aag ata caa gaa gtg tat atc cct ttc tct gct att tat aac act 192

47 Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr

48 50 55 60

50 caa gga ttt aag gag cct aat ata cag acg tat ctc tcc ggc tgt cca 240

51 Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro

52 65 70 75 80

54 ata aaa gca caa gtt ctg gaa gtg gaa cgc ttc aca tct aca aca agg 288

55 Ile Lys Ala Gln Val Leu Glu Val Glu Arg Phe Thr Ser Thr Thr Arg

56 85 90 95

58 gta cca agt att aat ctt tac act att gaa tta aca cat ggg gaa ttt 336

59 Val Pro Ser Ile Asn Leu Tyr Thr Ile Glu Leu Thr His Gly Glu Phe

60 100 105 110

62 aaa tgg caa gtt aag agg aaa ttc aag cat ttt caa gaa ttt cac aga 384

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING

DATE: 05/26/2006

PATENT APPLICATION: US/10/579,662

TIME: 08:27:02

Input Set : A:\133-PCT1-US1.ST25.txt

Output Set: N:\CRF4\05262006\J579662.raw

63	Lys	Trp	Gln	Val	Lys	Arg	Lys	Phe	Lys	His	Phe	Gln	Glu	Phe	His	Arg	
64			115					120				125					
66	gag	ctg	ctc	aag	tac	aaa	gcc	ttt	atc	cgc	atc	ccc	att	ccc	act	aga	432
67	Glu	Leu	Leu	Lys	Tyr	Lys	Ala	Phe	Ile	Arg	Ile	Pro	Ile	Pro	Thr	Arg	
68		130					135					140					
70	aga	cac	acg	ttt	agg	agg	caa	aac	gtc	aga	gag	gag	cct	cga	gag	atg	480
71	Arg	His	Thr	Phe	Arg	Arg	Gln	Asn	Val	Arg	Glu	Glu	Pro	Arg	Glu	Met	
72	145					150				155					160		
74	ccc	agt	ttg	ccc	cgt	tca	tct	gaa	aac	atg	ata	aga	gaa	gaa	caa	ttc	528
75	Pro	Ser	Leu	Pro	Arg	Ser	Ser	Glu	Asn	Met	Ile	Arg	Glu	Glu	Gln	Phe	
76				165				170				175					
78	ctt	ggt	aga	aga	aaa	caa	ctg	gaa	gat	tac	ttg	aca	aag	ata	cta	aaa	576
79	Leu	Gly	Arg	Arg	Lys	Gln	Leu	Glu	Asp	Tyr	Leu	Thr	Lys	Ile	Leu	Lys	
80			180					185				190					
82	atg	ccc	atg	tat	aga	aac	tat	cat	gcc	aca	aca	gag	ttt	ctt	gat	ata	624
83	Met	Pro	Met	Tyr	Arg	Asn	Tyr	His	Ala	Thr	Thr	Glu	Phe	Leu	Asp	Ile	
84		195					200					205					
86	agc	cag	ctg	tct	ttc	atc	cat	gat	ttg	gga	cca	aag	ggc	ata	gaa	ggt	672
87	Ser	Gln	Leu	Ser	Phe	Ile	His	Asp	Leu	Gly	Pro	Lys	Gly	Ile	Glu	Gly	
88		210				215					220						
90	atg	ata	atg	aaa	aga	tct	gga	gga	cac	aga	ata	cca	ggc	ttg	aat	tgc	720
91	Met	Ile	Met	Lys	Arg	Ser	Gly	Gly	His	Arg	Ile	Pro	Gly	Leu	Asn	Cys	
92	225				230				235						240		
94	tgt	ggt	cag	gga	aga	gcc	tgc	tac	aga	tgg	tca	aaa	aga	tgg	tta	ata	768
95	Cys	Gly	Gln	Gly	Arg	Ala	Cys	Tyr	Arg	Trp	Ser	Lys	Arg	Trp	Leu	Ile	
96			245					250				255					
98	gtg	aaa	gat	tcc	ttt	tta	ttg	tat	atg	aaa	cca	gac	agc	ggt	gcc	att	816
99	Val	Lys	Asp	Ser	Phe	Leu	Leu	Tyr	Met	Lys	Pro	Asp	Ser	Gly	Ala	Ile	
100			260					265				270					
102	gcc	ttc	gtc	ctg	ctg	gta	gac	aaa	gaa	ttc	aaa	att	aag	gtg	ggg	aag	864
103	Ala	Phe	Val	Leu	Leu	Val	Asp	Lys	Glu	Phe	Lys	Ile	Lys	Val	Gly	Lys	
104		275					280					285					
106	aag	gag	aca	gaa	acg	aaa	tat	gga	atc	cga	att	gat	aat	ctt	tca	agg	912
107	Lys	Glu	Thr	Glu	Thr	Lys	Tyr	Gly	Ile	Arg	Ile	Asp	Asn	Leu	Ser	Arg	
108		290				295					300						
110	aca	ctt	att	tta	aaa	tgc	aac	agc	tat	aga	cat	gct	cgg	tgg	tgg	gga	960
111	Thr	Leu	Ile	Leu	Lys	Cys	Asn	Ser	Tyr	Arg	His	Ala	Arg	Trp	Trp	Gly	
112	305				310				315			320					
114	ggg	gct	ata	gaa	gaa	ttc	atc	cag	aaa	cat	ggc	acc	aac	ttt	ctc	aaa	1008
115	Gly	Ala	Ile	Glu	Glu	Phe	Ile	Gln	Lys	His	Gly	Thr	Asn	Phe	Leu	Lys	
116			325					330				335					
118	gat	cat	cga	ttt	ggg	tca	tat	gct	gct	atc	caa	gag	aat	gct	tta	gct	1056
119	Asp	His	Arg	Phe	Gly	Ser	Tyr	Ala	Ala	Ile	Gln	Glu	Asn	Ala	Leu	Ala	
120			340					345				350					
122	aaa	tgg	tat	ggt	aat	gcc	aaa	gga	tat	ttt	gaa	gat	gtg	gca	aat	gca	1104
123	Lys	Trp	Tyr	Val	Asn	Ala	Lys	Gly	Tyr	Phe	Glu	Asp	Val	Ala	Asn	Ala	
124		355					360					365					
126	atg	gaa	gag	gca	aat	gaa	gag	att	ttt	atc	aca	gac	tgg	tgg	ctg	agt	1152
127	Met	Glu	Glu	Ala	Asn	Glu	Glu	Ile	Phe	Ile	Thr	Asp	Trp	Trp	Leu	Ser	

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128	370	375	380	
130	cca gaa atc ttc ctg aaa cgc cca gtg gtt gag gga aat cgt tgg agg	1200		
131	Pro Glu Ile Phe Leu Lys Arg Pro Val Val Glu Gly Asn Arg Trp Arg			
132	385 390 395 400			
134	ttg gac tgc att ctt aaa cga aaa gca caa caa gga gtg agg atc ttc	1248		
135	Leu Asp Cys Ile Leu Lys Arg Lys Ala Gln Gln Gly Val Arg Ile Phe			
136	405 410 415			
138	ata atg ctc tac aaa gag gtg gaa ctc gct ctt ggc atc aat agt gaa	1296		
139	Ile Met Leu Tyr Lys Glu Val Glu Leu Ala Leu Gly Ile Asn Ser Glu			
140	420 425 430			
142	tac acc aag agg act ttg atg cgt cta cat ccc aac ata aag gtg atg	1344		
143	Tyr Thr Lys Arg Thr Leu Met Arg Leu His Pro Asn Ile Lys Val Met			
144	435 440 445			
146	aga cac ccg gat cat gtg tca tcc acc gtc tat ttg tgg gct cac cat	1392		
147	Arg His Pro Asp His Val Ser Ser Thr Val Tyr Leu Trp Ala His His			
148	450 455 460			
150	gag aag ctt gtc atc att gac caa tcg gtg gcc ttt gtg gga ggg att	1440		
151	Glu Lys Leu Val Ile Ile Asp Gln Ser Val Ala Phe Val Gly Gly Ile			
152	465 470 475 480			
154	gac ctg gcc tat gga agg tgg gac gac aat gag cac aga ctc aca gac	1488		
155	Asp Leu Ala Tyr Gly Arg Trp Asp Asp Asn Glu His Arg Leu Thr Asp			
156	485 490 495			
158	gtg ggc agt gtg aag cgg gtc act tca gga ccg tct ctg ggt tcc ctc	1536		
159	Val Gly Ser Val Lys Arg Val Thr Ser Gly Pro Ser Leu Gly Ser Leu			
160	500 505 510			
162	cca cct gcc gca atg gag tct atg gaa tcc tta aga ctc aaa gat aaa	1584		
163	Pro Pro Ala Ala Met Glu Ser Met Glu Ser Leu Arg Leu Lys Asp Lys			
164	515 520 525			
166	aat gag cct gtt caa aac cta ccc atc cag aag agt att gat gat gtg	1632		
167	Asn Glu Pro Val Gln Asn Leu Pro Ile Gln Lys Ser Ile Asp Asp Val			
168	530 535 540			
170	gat tca aaa ctg aaa gga ata gga aag cca aga aag ttc tcc aaa ttt	1680		
171	Asp Ser Lys Leu Lys Gly Ile Gly Lys Pro Arg Lys Phe Ser Lys Phe			
172	545 550 555 560			
174	agt ctc tac aag cag ctc cac agg cac cac ctg cac gac gca gat agc	1728		
175	Ser Leu Tyr Lys Gln Leu His Arg His His Leu His Asp Ala Asp Ser			
176	565 570 575			
178	atc agc agc att gac agc acc tcc agt tat ttt aat cac tat aga agt	1776		
179	Ile Ser Ser Ile Asp Ser Thr Ser Ser Tyr Phe Asn His Tyr Arg Ser			
180	580 585 590			
182	cat cac aat tta atc cat ggt tta aaa ccc cac ttc aaa ctc ttt cac	1824		
183	His His Asn Leu Ile His Gly Leu Lys Pro His Phe Lys Leu Phe His			
184	595 600 605			
186	ccg tcc agt gag tct gag caa gga ctc act aga cct cat gct gat acc	1872		
187	Pro Ser Ser Glu Ser Glu Gln Gly Leu Thr Arg Pro His Ala Asp Thr			
188	610 615 620			
190	ggg tcc atc cgt agt tta cag aca ggt gtg gga gag ctg cat ggg gaa	1920		
191	Gly Ser Ile Arg Ser Leu Gln Thr Gly Val Gly Glu Leu His Gly Glu			
192	625 630 635 640			

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194	acc	aga	ttc	tgg	cat	gga	aag	gac	tac	tgc	aat	ttc	gtc	ttc	aaa	gac	1968
195	Thr	Arg	Phe	Trp	His	Gly	Lys	Asp	Tyr	Cys	Asn	Phe	Val	Phe	Lys	Asp	
196					645					650					655		
198	tgg	gtt	caa	ctt	gat	aaa	cct	ttt	gct	gat	ttc	att	gac	agg	tac	tcc	2016
199	Trp	Val	Gln	Leu	Asp	Lys	Pro	Phe	Ala	Asp	Phe	Ile	Asp	Arg	Tyr	Ser	
200				660					665						670		
202	acg	ccc	cgg	atg	ccc	tgg	cat	gac	att	gcc	tct	gca	gtc	cac	ggg	aag	2064
203	Thr	Pro	Arg	Met	Pro	Trp	His	Asp	Ile	Ala	Ser	Ala	Val	His	Gly	Lys	
204				675				680							685		
206	gcg	gct	cgt	gat	gtg	gca	cgt	cac	ttc	atc	cag	cgc	tgg	aac	ttc	aca	2112
207	Ala	Ala	Arg	Asp	Val	Ala	Arg	His	Phe	Ile	Gln	Arg	Trp	Asn	Phe	Thr	
208				690				695							700		
210	aaa	att	atg	aaa	tca	aaa	tat	cgg	tcc	ctt	tct	tat	cct	ttt	ctg	ctt	2160
211	Lys	Ile	Met	Lys	Ser	Lys	Tyr	Arg	Ser	Leu	Ser	Tyr	Pro	Phe	Leu	Leu	
212	705					710					715				720		
214	cca	aag	tct	caa	aca	aca	gcc	cat	gag	ttg	aga	tat	caa	gtg	cct	ggg	2208
215	Pro	Lys	Ser	Gln	Thr	Thr	Ala	His	Glu	Leu	Arg	Tyr	Gln	Val	Pro	Gly	
216				725						730					735		
218	tct	gtc	cat	gct	aac	gta	cag	ttg	ctc	cgc	tct	gct	gct	gat	tgg	tct	2256
219	Ser	Val	His	Ala	Asn	Val	Gln	Leu	Leu	Arg	Ser	Ala	Ala	Asp	Trp	Ser	
220				740					745						750		
222	gct	ggt	ata	aag	tac	cat	gaa	gag	tcc	atc	cac	gcc	gct	tac	gtc	cat	2304
223	Ala	Gly	Ile	Lys	Tyr	His	Glu	Glu	Ser	Ile	His	Ala	Ala	Tyr	Val	His	
224				755				760							765		
226	gtg	ata	gag	aac	agc	agg	cac	tat	atc	tat	atc	gaa	aac	cag	ttt	ttc	2352
227	Val	Ile	Glu	Asn	Ser	Arg	His	Tyr	Ile	Tyr	Ile	Glu	Asn	Gln	Phe	Phe	
228				770				775							780		
230	ata	agc	tgt	gct	gat	gac	aaa	ggt	gtg	ttc	aac	aag	ata	ggc	gat	gcc	2400
231	Ile	Ser	Cys	Ala	Asp	Asp	Lys	Val	Val	Phe	Asn	Lys	Ile	Gly	Asp	Ala	
232	785					790					795				800		
234	att	gcc	cag	agg	atc	ctg	aaa	gct	cac	agg	gaa	aac	cag	aaa	tac	cgg	2448
235	Ile	Ala	Gln	Arg	Ile	Leu	Lys	Ala	His	Arg	Glu	Asn	Gln	Lys	Tyr	Arg	
236				805						810					815		
238	gta	tat	gtc	gtg	ata	cca	ctt	ctg	cca	ggg	ttc	gaa	gga	gac	att	tca	2496
239	Val	Tyr	Val	Val	Ile	Pro	Leu	Leu	Pro	Gly	Phe	Glu	Gly	Asp	Ile	Ser	
240				820					825						830		
242	acc	ggc	gga	gga	aat	gct	cta	cag	gca	atc	atg	cac	ttc	aac	tac	aga	2544
243	Thr	Gly	Gly	Gly	Asn	Ala	Leu	Gln	Ala	Ile	Met	His	Phe	Asn	Tyr	Arg	
244				835				840							845		
246	acc	atg	tgc	aga	gga	gaa	aat	tcc	atc	ctt	gga	cag	tta	aaa	gca	gag	2592
247	Thr	Met	Cys	Arg	Gly	Glu	Asn	Ser	Ile	Leu	Gly	Gln	Leu	Lys	Ala	Glu	
248				850				855							860		
250	ctt	ggt	aat	cag	tgg	ata	aat	tac	ata	tca	ttc	tgt	ggt	ctt	aga	aca	2640
251	Leu	Gly	Asn	Gln	Trp	Ile	Asn	Tyr	Ile	Ser	Phe	Cys	Gly	Leu	Arg	Thr	
252	865					870					875				880		
254	cat	gca	gag	ctc	gaa	gga	aac	cta	gta	act	gag	ctt	atc	tat	gtc	cac	2688
255	His	Ala	Glu	Leu	Glu	Gly	Asn	Leu	Val	Thr	Glu	Leu	Ile	Tyr	Val	His	
256				885						890					895		
258	agc	aag	ttg	tta	att	gct	gat	gat	aac	act	ggt	att	att	ggc	tct	gcc	2736

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259 Ser Lys Leu Leu Ile Ala Asp Asp Asn Thr Val Ile Ile Gly Ser Ala
260          900          905          910
262 aac ata aat gac cgc agc atg ctg gga aag cgt gac agt gaa atg gct      2784
263 Asn Ile Asn Asp Arg Ser Met Leu Gly Lys Arg Asp Ser Glu Met Ala
264          915          920          925
266 gtc att gtg caa gat aca gag act gtt cct tca gta atg gat gga aaa      2832
267 Val Ile Val Gln Asp Thr Glu Thr Val Pro Ser Val Met Asp Gly Lys
268          930          935          940
270 gag tac caa gct ggc cgg ttt gcc cga gga ctt cgg cta cag tgc ttt      2880
271 Glu Tyr Gln Ala Gly Arg Phe Ala Arg Gly Leu Arg Leu Gln Cys Phe
272 945          950          955          960
274 agg gtt gtc ctt ggc tat ctt gat gac cca agt gag gac att cag gat      2928
275 Arg Val Val Leu Gly Tyr Leu Asp Asp Pro Ser Glu Asp Ile Gln Asp
276          965          970          975
278 cca gtg agt gac aaa ttc ttc aag gag gtg tgg gtt tca aca gca gct      2976
279 Pro Val Ser Asp Lys Phe Phe Lys Glu Val Trp Val Ser Thr Ala Ala
280          980          985          990
282 cga aat gct aca att tat gac aag gtt ttc cgg tgc ctt ccc aat gat      3024
283 Arg Asn Ala Thr Ile Tyr Asp Lys Val Phe Arg Cys Leu Pro Asn Asp
284          995          1000          1005
286 gaa gta cac aat tta att cag ctg aga gac ttt ata aac aag ccc      3069
287 Glu Val His Asn Leu Ile Gln Leu Arg Asp Phe Ile Asn Lys Pro
288          1010          1015          1020
290 gta tta gct aag gaa gat ccc att cga gct gag gag gaa ctg aag      3114
291 Val Leu Ala Lys Glu Asp Pro Ile Arg Ala Glu Glu Glu Leu Lys
292          1025          1030          1035
294 aag atc cgt gga ttt ttg gtg caa ttc ccc ttt tat ttc ttg tct      3159
295 Lys Ile Arg Gly Phe Leu Val Gln Phe Pro Phe Tyr Phe Leu Ser
296          1040          1045          1050
298 gaa gaa agc cta ctg cct tct gtt ggg acc aaa gag gcc ata gtg      3204
299 Glu Glu Ser Leu Leu Pro Ser Val Gly Thr Lys Glu Ala Ile Val
300          1055          1060          1065
302 ccc atg gag gtt tgg act taa      3225
303 Pro Met Glu Val Trp Thr
304          1070
307 <210> SEQ ID NO: 2
308 <211> LENGTH: 1074
309 <212> TYPE: PRT
310 <213> ORGANISM: Homo sapiens
312 <400> SEQUENCE: 2
314 Met Ser Leu Lys Asn Glu Pro Arg Val Asn Thr Ser Ala Leu Gln Lys
315 1          5          10          15
318 Ile Ala Ala Asp Met Ser Asn Ile Ile Glu Asn Leu Asp Thr Arg Glu
319          20          25          30
322 Leu His Phe Glu Gly Glu Glu Val Asp Tyr Asp Val Ser Pro Ser Asp
323          35          40          45
326 Pro Lys Ile Gln Glu Val Tyr Ile Pro Phe Ser Ala Ile Tyr Asn Thr
327          50          55          60
330 Gln Gly Phe Lys Glu Pro Asn Ile Gln Thr Tyr Leu Ser Gly Cys Pro

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,662

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Input Set : A:\133-PCT1-US1.ST25.txt

Output Set: N:\CRF4\05262006\J579662.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date